## SEQUENCE LISTING

(1) GENERAL INFORMATIO	TION:	INFORMA	GENERAL	(1)
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- (i) APPLICANT: Rezaie, Alireza
  - Esmon, Charles
- (ii) TITLE OF INVENTION: Calcium Binding Recombinant Antibody
  Against Protein C
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Patrea L. Pabst
  - (B) STREET: 1100 Peachtree Street, Suite 2800
  - (C) CITY: Atlanta
  - (D) STATE: Georgia
  - (E) COUNTRY: USA
  - (F) ZIP: 30309-4530
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US
  - (B) FILING DATE: Jun 9, 1994
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/982,832
  - (B) FILING DATE: 30-NOV-1992
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/730,040 (U.S. Patent No. 5,202,253)
  - (B) FILING DATE: 12-JUL-1991
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/292,447
  - (B) FILING DATE: 30-DEC-1988
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Pabst, Patrea L.
  - (B) REGISTRATION NUMBER: 31,284
  - (C) REFERENCE/DOCKET NUMBER: OMRF106CIP

- '(ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (404) 815-6508
  - (B) TELEFAX: (404) 815-6555
- (2) INFORMATION FOR SEQ ID NO:1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 12 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: NO
    - (v) FRAGMENT TYPE: Internal
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly Lys
1 5 10

- (2) INFORMATION FOR SEQ ID NO:2:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 40 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: YES
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

## AAGCGGCCGC TGGATAGACA GATGGGGGTG TCGTTTTGCC

- (2) INFORMATION FOR SEQ ID NO:3:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 30 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

## AAGCGGCCGC CCCCCCCCC

- (2) INFORMATION FOR SEQ ID NO:4:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 40 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: YES
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

## AAGCGGCCGC GAAGATGGAT ACAGTTGGTG CAGCATCAGC

- (2) INFORMATION FOR SEQ ID NO:5:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 28 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: NO
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

## AGGTTACTCT GCTCGAGTCT GGCCCTGG

- (2) INFORMATION FOR SEQ ID NO:6:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 36 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

## AGGCCTACTA GTTTACTAAC AATCCCTGGG CACAAT

- (2) INFORMATION FOR SEQ ID NO:7:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 37 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: NO
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

## TGTCCAGAGG AGAGCTCATT CTCACCCAGT CTCCGGC

- (2) INFORMATION FOR SEQ ID NO:8:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 34 base pairs
      - (B) TYPE: nucleic acid
      - (C) STRANDEDNESS: single
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: YES
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

## TCCTTCTAGA TTACTAACAC TCTCCCCTGT TGAA

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 417 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: HPC-4 Heavy Chain Variable Region (VH Gamma)
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_feature
    - (B) LOCATION: 1..57
- (D) OTHER INFORMATION: /note= "Signal peptide encoded by nucleotides 1 through 57."
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_feature
    - (B) LOCATION:  $58..\overline{4}17$
- (D) OTHER INFORMATION: /note= "Mature peptide encoded by nucleotides 58 through 417."
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGGGCAGGC TTTCTTCTTC ATTCTTGCTA CTG	ATTGCCC CTGCATATGT CCTGTCCCAG 60
GTTACTCTGA AAGAGTCTGG CCCTGGGATA TTG	CAGCCCT CCCAGACCCT CACTCTGACT 120
TGTTCTCTCT CTGGGTTTTC ACTGAGGACT TCT	GGTATGG GTGTAGGCTG GATTCGTCAG 180
CCTTCAGGGA AGGGTCTGGA GTGGCTGGCA CAC	ATTTGGT GGGATGATGA CAAGCGCTAT 240
AACCCAGTCC TGAAGAGCCG ACTGATAATC TCC	AAGGATA CCTCCAGGAA ACAGGTATTC 300
CTCAAGATCG CCAGTGTGGA CACTGCAGAT ACT	GCCACAT ACTACTGTGT TCGAATGATG 360
GATGATTACG ACGCTATGGA CTACTGGGGT CAA	GGAACCT CAGTCACCGT CTCCTCT 417

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 139 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
  - (iv) ANTI-SENSE: NO
  - (v) FRAGMENT TYPE: Internal
  - (vi) ORIGINAL SOURCE:
    - (A) ORGANISM: HPC-4 Heavy Chain Variable Region (VH Gamma)
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_feature
    - (B) LOCATION:  $20..\overline{139}$
- (D) OTHER INFORMATION: /note= "Gln at position 20 starts mature peptide."
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Gly Arg Leu Ser Ser Ser Phe Leu Leu Leu Ile Ala Pro Ala Tyr 1 5 10 15

Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln
20 25 30

Pro Ser Gln Thr Leu Thr Leu Thr Cys Ser Leu Ser Gly Phe Ser Leu 35 40 45

Arg Thr Ser Gly Met Gly Val Gly Trp Ile Arg Gln Pro Ser Gly Lys 50 55 60

Gly Leu Glu Trp Leu Ala His Ile Trp Trp Asp Asp Asp Lys Arg Tyr 65 70 75 80

Asn Pro Val Leu Lys Ser Arg Leu Ile Ile Ser Lys Asp Thr Ser Arg 85 90 95 Lys Gln Val Phe Leu Lys Ile Ala Ser Val Asp Thr Ala Asp Thr Ala 105 110 100 Thr Tyr Tyr Cys Val Arg Met Met Asp Asp Tyr Asp Ala Met Asp Tyr 120 Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser

- (2) INFORMATION FOR SEQ ID NO:11:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 387 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA
  - (iii) HYPOTHETICAL: NO
    - (iv) ANTI-SENSE: NO
    - (vi) ORIGINAL SOURCE:
      - (A) ORGANISM: HPC-4 Light Chain Variable Region (VL Kappa)
    - (ix) FEATURE:
      - (A) NAME/KEY: misc feature
      - (B) LOCATION:  $1..6\overline{6}$
- (D) OTHER INFORMATION: /note= "Signal peptide encoded by nucleotides 1 through 66."
  - (ix) FEATURE:
    - (A) NAME/KEY: misc feature
    - (B) LOCATION:  $67..\overline{3}87$
- (D) OTHER INFORMATION: /note= "Mature peptide encoded by nucleotides 67 through 387."
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGGATTTTC AGGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCCTCAGT CATAATGTCC 60 AGAGGACAAA TTATTCTCAC CCAGTCTCCG GCAATCATGT CTGCATCTCT GGGGGAGGAG 120 ATCACCCTAA CCTGCAGTGC CACTTCGAGT GTAACTTACG TCCACTGGTA CCAGCAGAAG 180

TCAGGCACTT CTC	CCAAACT CTTGA	ATTTAT GGGAC	CATCCA ACCTG	GCTTC TGGAGT	CCCT 240
TCTCGTTTCA GTO	GCAGTGG GTCT	GGACC TTTT	ATTCTC TCACA	GTCAG CAGTGT	GGAG 300
GCTGAAGATG CTC	CCGATTA TTAC	rgccat cagto	GAATA GTTAT	CCGCA CACGTT	CGGA 360
GGGGGGACCA AG	TGGAAAT AAAA	CGG			387
(A) (B) (C) (D) (ii) MOLE (iii) HYPO (iv) ANTI (v) FRAG (vi) ORIG (A) (ix) FEAT (A)	ENCE CHARACTE LENGTH: 129 TYPE: amino STRANDEDNESS TOPOLOGY: li CULE TYPE: pe THETICAL: NO -SENSE: NO MENT TYPE: N- INAL SOURCE: ORGANISM: HP	RISTICS: amino acids acid : single near ptide  terminal C-4 Light C sc_feature			
peptide."	ENCE DESCRIPT				
•	Phe Gln Val G 5			Leu Ile Ser	Ala Ser 15
Val Ile	Met Ser Arg 0 20	ly Gln Ile	Ile Leu Thr 25	Gln Ser Pro 30	Ala Ile
Met Ser	Ala Ser Leu G 35	Gly Glu Glu 40	Ile Thr Leu	Thr Cys Ser 45	Ala Thr

Ser Ser Val Thr Tyr Val His Trp Tyr Gln Gln Lys Ser Gly Thr Ser 50 55 60

Pro Lys Leu Leu Ile Tyr Gly Thr Ser Asn Leu Ala Ser Gly Val Pro 65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Phe Tyr Ser Leu Thr Val 85 90 95

Ser Ser Val Glu Ala Glu Asp Ala Ala Asp Tyr Tyr Cys His Gln Trp 100 105 110

Asn Ser Tyr Pro His Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys 115 120 125

Arg

## SEQUENCE LISTING



## (1) GENERAL INFORMATION:

(i) APPLICANT: Rezaie, Alireza Esmon, Charles Calcium Binding Recombinant Antibody Against Protein C (ii) TITLE OF INVENTION:

## (iii) NUMBER OF SEQUENCES: 12

## (iv) CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Pabst B

Suite 2800 STREET: 1100 Peachtree Street,

CITY: Atlanta <u>υ</u>

STATE: Georgia (D)

COUNTRY: USA

ZIP: 30309-4530 (E)

## (v) COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk (A)

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS (B)

SOFTWARE: PatentIn Release #1.0, Version #1.25 ς <u>(a)</u>

## CURRENT APPLICATION DATA: (vi)

(A) APPLICATION NUMBER: US

FILING DATE: (C)

CLASSIFICATION:

# (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/982,832 (B) FILING DATE: 30-NOV-1992

# (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/730,040 (U.S. Patent No. 5,202,253)

- (B) FILING DATE: 12-JUL-1991
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: US 07/292,447 (B) FILING DATE: 30-DEC-1988
- (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAMÉ: Pabst, Patrea L.(B) REGISTRATION NUMBER: 31,284(C) REFERENCE/DOCKET NUMBER: OMRF106CIP
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (404) 815-6508
  - (B) TELEFAX: (404) 815-6555
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12 amino acids (B) TYPE: amino acids
- STRANDEDNESS: single (C)
  - TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) FRAGMENT TYPE: Internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- Glu Asp Gln Val Asp Pro Arg Leu Ile Asp Gly Lys 1

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 40 base pairs

TYPE: nucleic acid STRANDEDNESS: single (B) TYPE: nucleic action (C) STRANDEDNESS: sir(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAGCGGCCGC TGGATAGACA GATGGGGGTG TCGTTTTGCC

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGCGGCCGC CCCCCCCC CCCCCCCCC

30

(2) INFORMATION FOR SEQ ID NO:4:

40

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AAGCGGCCGC GAAGATGGAT ACAGTTGGTG CAGCATCAGC

40

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

STRANDEDNESS: single TYPE: nucleic acid (B) TYPE: nucleic ac (C) STRANDEDNESS: sin (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGTTACTCT GCTCGAGTCT GGCCCTGG

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

28

LENGTH: 36 base pairs 

STRANDEDNESS: single TYPE: nucleic acid

TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGGCCTACTA GTTTACTAAC AATCCCTGGG CACAAT

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

STRANDEDNESS: single TYPE: nucleic acid

TOPOLOGY: linear (0)

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TGTCCAGAGG AGAGCTCATT CTCACCCAGT CTCCGGC

(2) INFORMATION FOR SEQ ID NO:8:

(A) LENGTH: 34 base pairs (i) SEQUENCE CHARACTERISTICS:

37

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- (B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TCCTTCTAGA TTACTAACAC TCTCCCCTGT TGAA

34

- (2) INFORMATION FOR SEQ ID NO:9:
- (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 417 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: HPC-4 Heavy Chain Variable Region (VH Gamma)
- FEATURE: (ix)
- (A) NAME/KEY: misc\_feature (B) LOCATION: 1..57 (D) OTHER INFORMATION: /note= "Signal peptide encoded by nucleotides 1 through

57."

<pre>(ix) FEATURE:     (A) NAME/KEY: misc feature     (B) LOCATION: 58417     (B) LOCATION: 58417</pre>	meleotides 58 through
Other intornation, / hoce hacute perciae	)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
ATGGGCAGGC TITCTICITC ATTCTTGCTA CTGATTGCCC CTGCATATGT CCTGTCCCAG	09
GTTACTCTGA AAGAGTCTGG CCCTGGGATA TTGCAGCCCT CCCAGACCCT CACTCTGACT	120
TGTTCTCTCT CTGGGTTTTC ACTGAGGACT TCTGGTATGG GTGTAGGCTG GATTCGTCAG	180
CCTTCAGGGA AGGGTCTGGA GTGGCTGGCA CACATTTGGT GGGATGATGA CAAGCGCTAT	240
AACCCAGTCC TGAAGAGCCG ACTGATAATC TCCAAGGATA CCTCCAGGAA ACAGGTATTC	300
CTCAAGATCG CCAGTGTGGA CACTGCAGAT ACTGCCACAT ACTACTGTGT TCGAATGATG	360
GATGATTACG ACGCTATGGA CTACTGGGGT CAAGGAACCT CAGTCACCGT CTCCTCT	417
(2) INFORMATION FOR SEQ ID NO:10:	
(i) SEQUENCE CHARACTERISTICS:     (A) LENGTH: 139 amino acids     (B) TYPE: amino acid     (C) STRANDEDNESS: single     (D) TOPOLOGY: linear	· <del>-</del> .
(ii) MOLECULE TYPE: peptide	
(iii) HYPOTHETICAL: NO	
(iv) ANTI-SENSE: NO	
(v) FRAGMENT TYPE: Internal	

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HPC-4 Heavy Chain Variable Region (VH Gamma)

FEATURE: (ix)

(A) NAME/KEY: misc feature (B) LOCATION: 20..139 (D) OTHER INFORMATION: /not

OTHER INFORMATION: /note= "Gln at position 20 starts mature peptide."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Tyr Met Gly Arg Leu Ser Ser Ser Phe Leu Leu Leu Ile Ala Pro Ala 1 Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln 25 Val Leu Ser

Gly Phe Ser Leu 45 Gln Thr Leu Thr Leu Thr Cys Ser Leu Ser 40

Ser

Pro

Arg

Lys G1yGln Pro Ser 60 Gly Trp Ile Arg Gly Val Gly Met Ser Thr 50

Tyr 80 Arg Trp Trp Asp Asp Asp Lys Ile Gly Leu Glu Trp Leu Ala His 65

Arg Ser Ile Ser Lys Asp Thr Ser Arg Leu Ile Asn Pro Val Leu Lys 85

Ala Thr Asp 110 Ser Val Asp Thr Ala 105 Phe Leu Lys Ile Ala 100 Lys Gln Val

TYrTyr Asp Ala Met Asp 125 Met Asp Asp 120 Arg Met Cys Val  $\frac{\text{Tyr}}{115}$ Tyr $\mathtt{Thr}$ 

Ser Thr Val Ser Trp Gly Gln Gly Thr Ser Val 130

(2) INFORMATION FOR SEQ ID NO:11:			
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 387 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>			
(ii) MOLECULE TYPE: DNA			
(iii) HYPOTHETICAL: NO			
(iv) ANTI-SENSE: NO			
(vi) ORIGINAL SOURCE: (A) ORGANISM: HPC-4 Light Chain Variable Region (VL Kappa)	le Region	(VL Kappa)	
<pre>(ix) FEATURE:     (A) NAME/KEY: misc_feature     (B) LOCATION: 166     (D) OTHER INFORMATION: /note= "Signal peptide encoded by nucleotides 66."</pre>	peptide e	ncoded by nuc	eleotides 1 through
<pre>(ix) FEATURE:     (A) NAME/KEY: misc feature     (B) LOCATION: 67387     (D) OTHER INFORMATION: /note= "Mature peptide encoded" 387."</pre>	peptide e	encoded by nucleotides	leotides 67 through
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:			
ATGGATTTTC AGGTGCAGAT TTTCAGCTTC CTGCTAATCA GTGCCTCAGT CATAATGTCC	CTCAGT CA	TAATGTCC	09
AGAGGACAAA TTATTCTCAC CCAGTCTCCG GCAATCATGT CTGCATCTCT GGGGGAGGAG	ATCTCT GG	GGGAGGAG	120
ATCACCCTAA CCTGCAGTGC CACTTCGAGT GTAACTTACG TCCACTGGTA CCAGCAGA	CTGGTA CC	CCAGCAGAAG	180

TCAGGCAC	TCAGGCACTT CTCCCAAACT CTTGATTTAT GGGACATCCA ACCTGGCTTC TGGAGTCCCT	240
TCTCGTTT	TCTCGTTTCA GTGGCAGTGG GTCTGGGACC TTTTATTCTC TCACAGTCAG CAGTGTGGAG	300
GCTGAAGATG	CTGCCGATTA TTACTGCCAT CAGTGGAATA GTTATCCGCA CACGTTCGGA	360
GGGGGGAC	GGGGGGACCA AGCTGGAAAT AAAACGG	387
(2) INFO	(2) INFORMATION FOR SEQ ID NO:12:	
(i)	(i) SEQUENCE CHARACTERISTICS:     (A) LENGTH: 129 amino acids     (B) TYPE: amino acid     (C) STRANDEDNESS: single     (D) TOPOLOGY: linear	
(ii)	(ii) MOLECULE TYPE: peptide	
(iii)	HYPOTHETICAL: NO	
(iv)	ANTI-SENSE: NO	
(v)	FRAGMENT TYPE: N-terminal	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: HPC-4 Light Chain Variable Region (VL Kappa)	
(ix)	<pre>(ix) FEATURE:     (A) NAME/KEY: misc feature     (B) LOCATION: 23129     (D) OTHER INFORMATION: /note= "Gln at position 23 starts mature</pre>	ure peptid
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:12:	
Met 1	Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser 1 5 15	

Tyr Gly Thr Ser Asn Leu Ala Ser Gly Val Pro 70  $\,$ Val Ile Met Ser Arg Gly Gln Ile Ile Leu Thr Gln Ser Pro Ala Ile 20 30 Ala Ser Leu Gly Glu Glu Ile Thr Leu Thr Cys Ser Ala Thr 35 45 Val Glu Ala Glu Asp Ala Asp Tyr Tyr Cys His Gln Trp 100 110 Tyr Pro His Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys 115 Trp Tyr Gln Gln Lys Ser Gly Thr 60 Ser Gly Ser Gly Thr Phe Tyr Ser Leu Thr 90 His' 55 Ser Val Thr Tyr Val 50 Pro Lys Leu Leu Ile 65 Ser Arg Phe Ser Gly 85 Ser Ser Val Ser Asn Ser Ser Met

Arg